SEQUENCE LISTING

```
<110> Ding, Jeak Ling
      Ho, Bow
      National University of Singapore

<120> Sushi Peptide Multimer

<130> 040184-000400US

<140> US 10/563,551
<141> 2006-01-04

<150> CA 2,432,972
<151> 2003-07-04

<150> WO PCT/SG04/00194
<151> 2004-07-02

<160> 11

<170> PatentIn Ver. 2.1

<210> 1
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      34-mer Sushi-3 peptide (S3 peptide), residues
      268-301 of Factor C, Sushi3 domain, LPS-binding
      motif

<400> 1
His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln
 1               5                  10                  15

Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
            20                  25                  30

Leu Met


<210> 2
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
      34-mer Sushi-3delta peptide (S3delta peptide)

<400> 2
His Ala Glu His Lys Val Lys Ile Lys Val Lys Gln Lys Tyr Gly Gln
 1               5                  10                  15

Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
            20                  25                  30

Leu Met
```

```
<210> 3
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:LPS-binding
      motif S3 PCR amplification forward primer

<400> 3
tcgaagacgg ccccaggatc cccatgctga acacaagg                              38


<210> 4
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:LPS-binding
      motif S3 PCR amplification reverse primer

<400> 4
tagaagaccc gggggtccat caaagaaagt agtta                                 35


<210> 5
<211> 3448
<212> DNA
<213> Carcinoscorpius rotundicauda

<220>
<223> Factor C cDNA

<220>
<221> CDS
<222> (18)..(3077)
<223> Factor C

<400> 5
gtgaaggtaa cttaagt atg gtc tta gcg tcg ttt ttg gtg tct ggt tta       50
                    Met Val Leu Ala Ser Phe Leu Val Ser Gly Leu
                     1               5                  10

gtt cta ggg cta cta gcc caa aaa atg cgc cca gtt cag tcc aaa gga      98
Val Leu Gly Leu Leu Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly
             15                  20                  25

gta gat cta ggc ttg tgt gat gaa acg agg ttc gag tgt aag tgt ggc      146
Val Asp Leu Gly Leu Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly
         30                  35                  40

gat cca ggc tat gtg ttc aac att cca gtg aaa caa tgt aca tac ttt      194
Asp Pro Gly Tyr Val Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe
     45                  50                  55

tat cga tgg agg ccg tat tgt aaa cca tgt gat gac ctg gag gct aag      242
Tyr Arg Trp Arg Pro Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys
 60                  65                  70                  75
```

```
gat att tgt cca aag tac aaa cga tgt caa gag tgt aag gct ggt ctt    290
Asp Ile Cys Pro Lys Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu
            80                  85                  90

gat agt tgt gtt act tgt cca cct aac aaa tat ggt act tgg tgt agc    338
Asp Ser Cys Val Thr Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser
            95                 100                 105

ggt gaa tgt cag tgt aag aat gga ggt atc tgt gac cag agg aca gga    386
Gly Glu Cys Gln Cys Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly
        110                 115                 120

gct tgt gca tgt cgt gac aga tat gaa ggg gtg cac tgt gaa att ctc    434
Ala Cys Ala Cys Arg Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu
        125                 130                 135

aaa ggt tgt cct ctt ctt cca tcg gat tct cag gtt cag gaa gtc aga    482
Lys Gly Cys Pro Leu Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg
140                 145                 150                 155

aat cca cca gat aat ccc caa act att gac tac agc tgt tca cca ggg    530
Asn Pro Pro Asp Asn Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly
                160                 165                 170

ttc aag ctt aag ggt atg gca cga att agc tgt ctc cca aat gga cag    578
Phe Lys Leu Lys Gly Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln
            175                 180                 185

tgg agt aac ttt cca ccc aaa tgt att cga gaa tgt gcc atg gtt tca    626
Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser
            190                 195                 200

tct cca gaa cat ggg aaa gtg aat gct ctt agt ggt gat atg ata gaa    674
Ser Pro Glu His Gly Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu
        205                 210                 215

ggg gct act tta cgg ttc tca tgt gat agt ccc tac tac ttg att ggt    722
Gly Ala Thr Leu Arg Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly
220                 225                 230                 235

caa gaa aca tta acc tgt cag ggt aat ggt cag tgg aat gga cag ata    770
Gln Glu Thr Leu Thr Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile
                240                 245                 250

cca caa tgt aag aac ttg gtc ttc tgt cct gac ctg gat cct gta aac    818
Pro Gln Cys Lys Asn Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn
            255                 260                 265

cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat ggt cag    866
His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln
        270                 275                 280

ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac tac ttc    914
Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
        285                 290                 295

ttg atg ggt ttt gac acc tta aaa tgt aac cct gat ggg tct tgg tca    962
Leu Met Gly Phe Asp Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser
300                 305                 310                 315
```

```
gga tca cag cca tcc tgt gtt aaa gtg gca gac aga gag gtc gac tgt    1010
Gly Ser Gln Pro Ser Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys
            320                 325                 330

gac agt aaa gct gta gac ttc ttg gat gat gtt ggt gaa cct gtc agg    1058
Asp Ser Lys Ala Val Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg
            335                 340                 345

atc cac tgt cct gct ggc tgt tct ttg aca gct ggt act gtg tgg ggt    1106
Ile His Cys Pro Ala Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly
            350                 355                 360

aca gcc ata tac cat gaa ctt tcc tca gtg tgt cgt gca gcc atc cat    1154
Thr Ala Ile Tyr His Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His
            365                 370                 375

gct ggc aag ctt cca aac tct gga gga gcg gtg cat gtt gtg aac aat    1202
Ala Gly Lys Leu Pro Asn Ser Gly Gly Ala Val His Val Val Asn Asn
380                 385                 390                 395

ggc ccc tac tcg gac ttt ctg ggt agt gac ctg aat ggg ata aaa tcg    1250
Gly Pro Tyr Ser Asp Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser
                400                 405                 410

gaa gag ttg aag tct ctt gcc cgg agt ttc cga ttc gat tat gtc cgt    1298
Glu Glu Leu Lys Ser Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg
            415                 420                 425

tcc tcc aca gca ggt aaa tca gga tgt cct gat gga tgg ttt gag gta    1346
Ser Ser Thr Ala Gly Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val
            430                 435                 440

gac gag aac tgt gtg tac gtt aca tca aaa cag aga gcc tgg gaa aga    1394
Asp Glu Asn Cys Val Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg
    445                 450                 455

gct caa ggt gtg tgt acc aat atg gct gct cgt ctt gct gtg ctg gac    1442
Ala Gln Gly Val Cys Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp
460                 465                 470                 475

aaa gat gta att cca aat tcg ttg act gag act cta cga ggg aaa ggg    1490
Lys Asp Val Ile Pro Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly
                480                 485                 490

tta aca acc acg tgg ata gga ttg cac aga cta gat gct gag aag ccc    1538
Leu Thr Thr Thr Trp Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro
            495                 500                 505

ttt att tgg gag tta atg gat cgt agt aat gtg gtt ctg aat gat aac    1586
Phe Ile Trp Glu Leu Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn
            510                 515                 520

cta aca ttc tgg gcc tct ggc gaa cct gga aat gaa act aac tgt gta    1634
Leu Thr Phe Trp Ala Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val
            525                 530                 535

tat atg gac atc caa gat cag ttg cag tct gtg tgg aaa acc aag tca    1682
Tyr Met Asp Ile Gln Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser
540                 545                 550                 555
```

```
tgt ttt cag ccc tca agt ttt gct tgc atg atg gat ctg tca gac aga    1730
Cys Phe Gln Pro Ser Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg
            560             565             570

aat aaa gcc aaa tgc gat gat cct gga tca ctg gaa aat gga cac gcc    1778
Asn Lys Ala Lys Cys Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala
            575             580             585

aca ctt cat gga caa agt att gat ggg ttc tat gct ggt tct tct ata    1826
Thr Leu His Gly Gln Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile
            590             595             600

agg tac agc tgt gag gtt ctc cac tac ctc agt gga act gaa acc gta    1874
Arg Tyr Ser Cys Glu Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val
            605             610             615

act tgt aca aca aat ggc aca tgg agt gct cct aaa cct cga tgt atc    1922
Thr Cys Thr Thr Asn Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile
620             625             630             635

aaa gtc atc acc tgc caa aac ccc cct gta cca tca tat ggt tct gtg    1970
Lys Val Ile Thr Cys Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val
            640             645             650

gaa atc aaa ccc cca agt cgg aca aac tcg ata agt cgt gtt ggg tca    2018
Glu Ile Lys Pro Pro Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser
            655             660             665

cct ttc ttg agg ttg cca cgg tta ccc ctc cca tta gct aga gca gcc    2066
Pro Phe Leu Arg Leu Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala
            670             675             680

aaa cct cct cca aaa cct aga tcc tca caa ccc tct act gtg gac ttg    2114
Lys Pro Pro Pro Lys Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu
            685             690             695

gct tct aaa gtt aaa cta cct gaa ggt cat tac cgg gta ggg tct cga    2162
Ala Ser Lys Val Lys Leu Pro Glu Gly His Tyr Arg Val Gly Ser Arg
700             705             710             715

gcc atc tac acg tgc gag tcg aga tac tac gaa cta ctt gga tct caa    2210
Ala Ile Tyr Thr Cys Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln
            720             725             730

ggc aga aga tgt gac tct aat gga aac tgg agt ggt cgg cca gcg agc    2258
Gly Arg Arg Cys Asp Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser
            735             740             745

tgt att cca gtt tgt gga cgg tca gac tct cct cgt tct cct ttt atc    2306
Cys Ile Pro Val Cys Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile
            750             755             760

tgg aat ggg aat tct aca gaa ata ggt cag tgg ccg tgg cag gca gga    2354
Trp Asn Gly Asn Ser Thr Glu Ile Gly Gln Trp Pro Trp Gln Ala Gly
            765             770             775

atc tct aga tgg ctt gca gac cac aat atg tgg ttt ctc cag tgt gga    2402
Ile Ser Arg Trp Leu Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly
780             785             790             795
```

```
gga tct cta ttg aat gag aaa tgg atc gtc act gct gcc cac tgt gtc    2450
Gly Ser Leu Leu Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val
            800             805                 810

acc tac tct gct act gct gag att att gac ccc aat cag ttt aaa atg    2498
Thr Tyr Ser Ala Thr Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met
            815             820                 825

tat ctg ggc aag tac tac cgt gat gac agt aga gac gat gac tat gta    2546
Tyr Leu Gly Lys Tyr Tyr Arg Asp Asp Ser Arg Asp Asp Asp Tyr Val
            830             835                 840

caa gta aga gag gct ctt gag atc cac gtg aat cct aac tac gac ccc    2594
Gln Val Arg Glu Ala Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro
            845             850                 855

ggc aat ctc aac ttt gac ata gcc cta att caa ctg aaa act cct gtt    2642
Gly Asn Leu Asn Phe Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val
860             865             870                 875

act ttg aca aca cga gtc caa cca atc tgt ctg cct act gac atc aca    2690
Thr Leu Thr Thr Arg Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr
            880             885                 890

aca aga gaa cac ttg aag gag gga aca tta gca gtg gtg aca ggt tgg    2738
Thr Arg Glu His Leu Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp
            895             900                 905

ggt ttg aat gaa aac aac acc tat tca gag acg att caa caa gct gtg    2786
Gly Leu Asn Glu Asn Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val
            910             915                 920

cta cct gtt gtt gca gcc agc acc tgt gaa gag ggg tac aag gaa gca    2834
Leu Pro Val Val Ala Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala
            925             930                 935

gac tta cca ctg aca gta aca gag aac atg ttc tgt gca ggt tac aag    2882
Asp Leu Pro Leu Thr Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys
940             945             950                 955

aag gga cgt tat gat gcc tgc agt ggg gac agt gga gga cct tta gtg    2930
Lys Gly Arg Tyr Asp Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val
            960             965                 970

ttt gct gat gat tcc cgt acc gaa agg cgg tgg gtc ttg gaa ggg att    2978
Phe Ala Asp Asp Ser Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile
            975             980                 985

gtc agc tgg ggc agt ccc agt gga tgt ggc aag gcg aac cag tac ggg    3026
Val Ser Trp Gly Ser Pro Ser Gly Cys Gly Lys Ala Asn Gln Tyr Gly
            990             995                 1000

ggc ttc act aaa gtt aac gtt ttc ctg tca tgg att agg cag ttc att    3074
Gly Phe Thr Lys Val Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile
1005                        1010                1015

tga aactgatcta aatattttaa gcatggttat aaacgtcttg tttcctatta        3127

1020

ttgctttact agtttaaccc ataagaaggt taactgggta aggcacaagg atcattgttt 3187
```

ctgtttgttt ttacaaatgg ttattttagt cagtgaatga gaatagtatc cattgaagac 3247

tgttaccttt tattctacct ttttatatta ctatgtaagt atttgggata tcttctacac 3307

atgaaaattc tgtcatttta ccataaattt ggtttctggt gtgtgctaag tccaccagta 3367

gagaacgatg taattttcac tagcacatga aataaatata gaacaaatct attataaact 3427

accttaaaaa aaaaaaaaaa a   3448

<210> 6
<211> 1019
<212> PRT
<213> Carcinoscorpius rotundicauda

<220>
<223> Factor C

<400> 6
Met Val Leu Ala Ser Phe Leu Val Ser Gly Leu Val Leu Gly Leu Leu
1   5   10   15
Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly Val Asp Leu Gly Leu
            20   25   30
Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly Asp Pro Gly Tyr Val
        35   40   45
Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe Tyr Arg Trp Arg Pro
    50   55   60
Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys Asp Ile Cys Pro Lys
65   70   75   80
Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu Asp Ser Cys Val Thr
            85   90   95
Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser Gly Glu Cys Gln Cys
            100   105   110
Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly Ala Cys Ala Cys Arg
        115   120   125
Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu Lys Gly Cys Pro Leu
    130   135   140
Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg Asn Pro Pro Asp Asn
145   150   155   160
Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly Phe Lys Leu Lys Gly
                165   170   175
Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln Trp Ser Asn Phe Pro
            180   185   190
Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser Ser Pro Glu His Gly
        195   200   205
Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu Gly Ala Thr Leu Arg
    210   215   220
Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly Gln Glu Thr Leu Thr
225   230   235   240
Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile Pro Gln Cys Lys Asn
            245   250   255
Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn His Ala Glu His Lys
            260   265   270
Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
    275   280   285
Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Gly Phe Asp
    290   295   300
Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser Gly Ser Gln Pro Ser
305   310   315   320

```
Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys Asp Ser Lys Ala Val
            325             330             335
Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg Ile His Cys Pro Ala
            340             345             350
Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly Thr Ala Ile Tyr His
            355             360             365
Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His Ala Gly Lys Leu Pro
    370             375             380
Asn Ser Gly Gly Ala Val His Val Val Asn Asn Gly Pro Tyr Ser Asp
385             390             395             400
Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser Glu Glu Leu Lys Ser
            405             410             415
Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg Ser Ser Thr Ala Gly
            420             425             430
Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val Asp Glu Asn Cys Val
            435             440             445
Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg Ala Gln Gly Val Cys
    450             455             460
Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp Lys Asp Val Ile Pro
465             470             475             480
Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly Leu Thr Thr Thr Trp
            485             490             495
Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro Phe Ile Trp Glu Leu
            500             505             510
Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn Leu Thr Phe Trp Ala
            515             520             525
Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val Tyr Met Asp Ile Gln
            530             535             540
Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser Cys Phe Gln Pro Ser
545             550             555             560
Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg Asn Lys Ala Lys Cys
            565             570             575
Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala Thr Leu His Gly Gln
            580             585             590
Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile Arg Tyr Ser Cys Glu
            595             600             605
Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val Thr Cys Thr Thr Asn
    610             615             620
Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile Lys Val Ile Thr Cys
625             630             635             640
Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val Glu Ile Lys Pro Pro
            645             650             655
Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser Pro Phe Leu Arg Leu
            660             665             670
Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala Lys Pro Pro Pro Lys
            675             680             685
Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu Ala Ser Lys Val Lys
            690             695             700
Leu Pro Glu Gly His Tyr Arg Val Gly Ser Arg Ala Ile Tyr Thr Cys
705             710             715             720
Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln Gly Arg Arg Cys Asp
            725             730             735
Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser Cys Ile Pro Val Cys
            740             745             750
Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile Trp Asn Gly Asn Ser
            755             760             765
Thr Glu Ile Gly Gln Trp Pro Trp Gln Ala Gly Ile Ser Arg Trp Leu
    770             775             780
Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly Gly Ser Leu Leu Asn
785             790             795             800
```

```
Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Thr Tyr Ser Ala Thr
            805                     810                 815
Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met Tyr Leu Gly Lys Tyr
            820                 825                 830
Tyr Arg Asp Asp Ser Arg Asp Asp Asp Tyr Val Gln Val Arg Glu Ala
            835                 840                 845
Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro Gly Asn Leu Asn Phe
        850                 855                 860
Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val Thr Leu Thr Thr Arg
865                 870                 875                 880
Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr Thr Arg Glu His Leu
                885                 890                 895
Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp Gly Leu Asn Glu Asn
            900                 905                 910
Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val Leu Pro Val Val Ala
        915                 920                 925
Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala Asp Leu Pro Leu Thr
    930                 935                 940
Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys Lys Gly Arg Tyr Asp
945                 950                 955                 960
Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Phe Ala Asp Asp Ser
            965                 970                 975
Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile Val Ser Trp Gly Ser
            980                 985                 990
Pro Ser Gly Cys Gly Lys Ala Asn Gln Tyr Gly Gly Phe Thr Lys Val
        995             1000                1005
Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile
    1010            1015
```

<210> 7
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:recombinant S3
      monomer (rS3-1mer) peptide, with additional Pro
      and Asp at ends from acid cleavage of rS3-4mer DP
      linker

<400> 7
```
Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly
 1               5               10                  15

Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr
            20                  25                  30

Phe Leu Met Asp
        35
```

<210> 8
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:recombinant S3
      tetramer (rS3-4mer) tandem repeat peptide with
      acid cleavable DP linker between S3 units

<220>
<221> CDS
<222> (1)..(468)
<223> rS3-4mer

<400> 8
```
ccc cag gat ccc cat gct gaa cac aag gtt aaa att ggt gtg gaa caa    48
Pro Gln Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln
 1               5                   10                  15

aaa tat ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg    96
Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser
            20                  25                  30

ggt aac tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag   144
Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
        35                  40                  45

gtt aaa att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act   192
Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
    50                  55                  60

gaa gtg acc tat acg tgt tcg ggt aac tac ttc ttg atg gac ccc cag   240
Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
65                  70                  75                  80

gat ccc cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat   288
Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
                85                  90                  95

ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac   336
Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
            100                 105                 110

tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag gtt aaa   384
Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
        115                 120                 125

att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act gaa gtg   432
Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
    130                 135                 140

acc tat acg tgt tcg ggt aac tac ttc ttg atg gac                   468
Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp
145                 150                 155
```

<210> 9
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:recombinant S3
      tetramer (rS3-4mer) tandem repeat peptide with
      acid cleavable DP linkerbetween S3 units

```
<400> 9
Pro Gln Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln
 1               5                  10                 15

Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser
                20                  25                 30

Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
            35                  40                 45

Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
    50                  55                 60

Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
65                  70                  75                 80

Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
                85                  90                 95

Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
            100                 105                110

Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
        115                 120                 125

Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
    130                 135                 140

Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp
145                 150                 155
```

```
<210> 10
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:amino acids
      used to link S3 multimer to remainder of
      polypeptide

<400> 10
Ile Glu Gly Arg
  1
```

```
<210> 11
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:enterokinase
      recognition sequence, enterokinase cleavage site

<220>
<221> MOD_RES
<222> (1)..(7)
<223> Xaa = any amino acid
```

```
<220>
<221> MOD_RES
<222> (4)..(5)
<223> Asp at positions 4 and 5 may be present or absent

<400> 11
Xaa Asp Asp Asp Asp Lys Xaa
  1                   5
```